

SEQUENCE LISTING

<110> Behl, Christian
Klostermann, Andreas

<120> Human semaphorin 6A-1 (SEMA6A-A), a gene involved
in neuronal development and regeneration mechanisms
during apoptosis, and its use as a potential drug target

<130> 48498-258443

<140> 09/856,681

<141> 2001-05-22

<150> PCT/EP99/09215

<151> 1999-11-26

<150> 98122441.3

<151> 1998-11-26

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<170> PatentIn Ver. 2.1

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96

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144

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192

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240

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Ile Asp Thr Ser His Thr Glu Glu Ile Tyr Cys Ser Lys Lys Leu Thr
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288

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Trp Lys Ser Arg Gln Ala Asp Val Asp Thr Cys Arg Met Lys Gly Lys	
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cat aag gat gag tgc cac aac ttt att aaa gtt ctt cta aag aaa aac	384
His Lys Asp Glu Cys His Asn Phe Ile Lys Val Leu Leu Lys Lys Asn	
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gat gat gca ttg ttt gtc tgt gga act aat gcc ttc aac cct tcc tgc	432
Asp Asp Ala Leu Phe Val Cys Gly Thr Asn Ala Phe Asn Pro Ser Cys	
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Ile Asp Ala Val Ile Tyr Arg Ser Leu Gly Glu Ser Pro Thr Leu Arg	
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Ser His Phe Tyr Phe Asn Ile Leu Gln Ala Val Thr Asp Val Ile Arg	
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Ile Asn Gly Arg Asp Val Val Leu Ala Thr Phe Ser Thr Pro Tyr Asn	
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agc atc cct ggg tct gca gtc tgt gcc tat gac atg ctt gac att gcc	1008
Ser Ile Pro Gly Ser Ala Val Cys Ala Tyr Asp Met Leu Asp Ile Ala	
325 330 335	

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Cys Ala Gly Ser Ser Leu Glu Arg Tyr Ala Thr Ser Asn Glu Phe				
cct gat gat acc ctg aac ttc atc aag acg cac ccg ctc atg gat gag	385	390	395	1200
Pro Asp Asp Thr Leu Asn Phe Ile Lys Thr His Pro Leu Met Asp Glu				
gca gtg ccc tcc atc ttc aac agg cca tgg ttc ctg aga aca atg gtc	405	410	415	1248
Ala Val Pro Ser Ile Phe Asn Arg Pro Trp Phe Leu Arg Thr Met Val				
aga tac cgc ctt acc aaa att gca gtg gac aca gct gct ggg cca tat	420	425	430	1296
Arg Tyr Arg Leu Thr Lys Ile Ala Val Asp Thr Ala Ala Gly Pro Tyr				
cag aat cac act gtg gtt ttt ctg gga tca gag aag gga atc atc ttg	435	440	445	1344
Gln Asn His Thr Val Val Phe Leu Gly Ser Glu Lys Gly Ile Ile Leu				
aag ttt ttg gcc aga ata gga aat agt ggt ttt cta aat gac agc ctt	450	455	460	1392
Lys Phe Leu Ala Arg Ile Gly Asn Ser Gly Phe Leu Asn Asp Ser Leu				
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Phe Leu Glu Glu Met Ser Val Tyr Asn Ser Glu Lys Cys Ser Tyr Asp				
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Gly Val Glu Asp Lys Arg Ile Met Gly Met Gln Leu Asp Arg Ala Ser				
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Ser Ser Leu Tyr Val Ala Phe Ser Thr Cys Val Ile Lys Val Pro Leu				
ggc cgg tgt gaa cga cat ggg aag tgt aaa aaa acc tgt att gcc tcc	515	520	525	1584
Gly Arg Cys Glu Arg His Gly Lys Cys Lys Lys Thr Cys Ile Ala Ser				
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Arg Asp Pro Tyr Cys Gly Trp Ile Lys Glu Gly Ala Cys Ser His				
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cat aat cac caa gac aag aag gga gtg att cgg gaa agt tac ctc aaa His Asn His Gln Asp Lys Lys Gly Val Ile Arg Glu Ser Tyr Leu Lys 625	630	635	1920
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gcc atc ctc acg cca ctc atg cac aac ggc aag ctc gcc act ccc ggc Ala Ile Leu Thr Pro Leu Met His Asn Gly Lys Leu Ala Thr Pro Gly 725	730	735	2208
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acg gcc ctc ccc acc cca gag tca acc cca acg ctg cag cag aag cgg Thr Ala Leu Pro Thr Pro Glu Ser Thr Pro Thr Leu Gln Gln Lys Arg 755	760	765	2304
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aat gcc tgc aca aag gac atg ccc ccc atg ggc tcc cct gtg att ccc Asn Ala Cys Thr Lys Asp Met Pro Pro Met Gly Ser Pro Val Ile Pro 785	790	795	2400

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Pro Lys Met Ser Glu Val Ala Gln Met Ala Leu Glu Asp Gln Ala Ala			
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cac cag gcc acc act ctc aaa aga aac aac act aac tcc tcc aat tcc	2832		
His Gln Ala Thr Thr Leu Lys Arg Asn Asn Thr Asn Ser Ser Asn Ser			
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tct cac ctc tcc aga aac cag agc ttt ggc agg gga gac aac ccg ccg	2880		
Ser His Leu Ser Arg Asn Gln Ser Phe Gly Arg Gly Asp Asn Pro Pro			
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ccc gcc ccg cag agg gtg gac tcc atc cag gtg cac agc tcc cag cca	2928		
Pro Ala Pro Gln Arg Val Asp Ser Ile Gln Val His Ser Ser Gln Pro			
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Asn Ser Leu Thr Arg Ser Gly Leu Lys Arg Thr Pro Ser Leu Lys Pro			
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gac gta ccc ccc aaa cca tcc ttt gct ccc ctt tcc aca tcc atg aag	3072		
Asp Val Pro Pro Lys Pro Ser Phe Ala Pro Leu Ser Thr Ser Met Lys			
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3093

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 50 55 60
 Asn Gly Thr Leu Tyr Ile Ala Ala Arg Asp His Ile Tyr Thr Val Asp
 65 70 75 80
 Ile Asp Thr Ser His Thr Glu Glu Ile Tyr Cys Ser Lys Lys Leu Thr
 85 90 95
 Trp Lys Ser Arg Gln Ala Asp Val Asp Thr Cys Arg Met Lys Gly Lys
 100 105 110
 His Lys Asp Glu Cys His Asn Phe Ile Lys Val Leu Lys Lys Asn
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 Asp Asp Ala Leu Phe Val Cys Gly Thr Asn Ala Phe Asn Pro Ser Cys
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 Arg Asn Tyr Lys Met Asp Thr Leu Glu Pro Phe Gly Asp Glu Phe Ser
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 Gly Met Ala Arg Cys Pro Tyr Asp Ala Lys His Ala Asn Val Ala Leu
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 Phe Ala Asp Gly Lys Leu Tyr Ser Ala Thr Val Thr Asp Phe Leu Ala
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 Thr Val Lys His Asp Ser Lys Trp Leu Lys Glu Pro Tyr Phe Val Gln
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 Ala Val Asp Tyr Gly Asp Tyr Ile Tyr Phe Phe Arg Glu Ile Ala
 225 230 235 240
 Val Glu Tyr Asn Thr Met Gly Lys Val Val Phe Pro Arg Val Ala Gln
 245 250 255

Val Cys Lys Asn Asp Met Gly Gly Ser Gln Arg Val Leu Glu Lys Gln
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 Trp Thr Ser Phe Leu Lys Ala Arg Leu Asn Cys Ser Val Pro Gly Asp
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 Ser Ile Pro Gly Ser Ala Val Cys Ala Tyr Asp Met Leu Asp Ile Ala
 325 330 335
 Ser Val Phe Thr Gly Arg Phe Lys Glu Gln Lys Ser Pro Asp Ser Thr
 340 345 350
 Trp Thr Pro Val Pro Asp Glu Arg Val Pro Lys Pro Arg Pro Gly Cys
 355 360 365
 Cys Ala Gly Ser Ser Ser Leu Glu Arg Tyr Ala Thr Ser Asn Glu Phe
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 Pro Asp Asp Thr Leu Asn Phe Ile Lys Thr His Pro Leu Met Asp Glu
 385 390 395 400
 Ala Val Pro Ser Ile Phe Asn Arg Pro Trp Phe Leu Arg Thr Met Val
 405 410 415
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 565 570 575

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 580 585 590
 Ala Gln Glu Gly Tyr Glu Ser Arg Gly Gly Met Leu Asp Trp Lys His
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 Leu Leu Asp Ser Pro Asp Ser Thr Asp Pro Leu Gly Ala Val Ser Ser
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 His Asn His Gln Asp Lys Lys Gly Val Ile Arg Glu Ser Tyr Leu Lys
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 Gly His Asp Gln Leu Val Pro Val Thr Leu Leu Ala Ile Ala Val Ile
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 Lys Glu Leu Thr His Ser Arg Arg Gly Ser Met Ser Ser Val Thr Lys
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 Gln Pro Ser Gly Gln Ala Val Thr Val Ser Arg Gln Pro Ser Leu Asn
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 Ala Tyr Asn Ser Leu Thr Arg Ser Gly Leu Lys Arg Thr Pro Ser Leu
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 aag ccg gac gta ccc ccc aaa cca tcc ttt qct ccc ctt tcc aca tcc 192
 Lys Pro Asp Val Pro Pro Lys Pro Ser Phe Ala Pro Leu Ser Thr Ser
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Gly His Asp Gln Leu Val Pro Val Thr Leu Leu Ala Ile Ala Val Ile	
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Val Cys Asp His Arg Arg Lys Asp Val Ala Val Val Gln Arg Lys Glu	
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Lys Glu Leu Thr His Ser Arg Arg Gly Ser Met Ser Val Thr Lys	
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Leu Ser Gly Leu Phe Gly Asp Thr Gln Ser Lys Asp Pro Lys Pro Glu	
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Asn Thr Ala Lys Met Leu Ile Lys Ala Asp Gln His His Leu Asp Leu	
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Val Leu Pro Ile Thr Gln Gln Gly Tyr Gln His Glu Tyr Val Asp Gln	
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Pro Lys Met Ser Glu Val Ala Gln Met Ala Leu Glu Asp Gln Ala Ala	
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Thr Leu Glu Tyr Lys Thr Ile Lys Glu His Leu Ser Ser Lys Ser Pro	
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Asn His Gly Val Asn Leu Val Glu Asn Leu Asp Ser Leu Pro Pro Lys	
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Val Pro Gln Arg Glu Ala Ser Leu Gly Pro Pro Gly Ala Ser Leu Ser	
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Gln Thr Gly Leu Ser Lys Arg Leu Glu Met His His Ser Ser Tyr	
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Gly Val Asp Tyr Lys Arg Ser Tyr Pro Thr Asn Ser Leu Thr Arg Ser	
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Ser His Leu Ser Arg Asn Gln Ser Phe Gly Arg Gly Asp Asn Pro Pro	
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 35 40 45

Asn Thr Thr Gln Arg His Arg Leu Asp Ile Gln Met Ile Met Ile Met
 50 55 60

Asn Gly Thr Leu Tyr Ile Ala Ala Arg Asp His Ile Tyr Thr Val Asp
 65 70 75 80

Ile Asp Thr Ser His Thr Glu Glu Ile Tyr Cys Ser Lys Lys Leu Thr
 85 90 95

Trp Lys Ser Arg Gln Ala Asp Val Asp Thr Cys Arg Met Lys Gly Lys
 100 105 110

His Lys Asp Glu Cys His Asn Phe Ile Lys Val Leu Leu Lys Lys Asn
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Asp Asp Ala Leu Phe Val Cys Gly Thr Asn Ala Phe Asn Pro Ser Cys
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Arg Asn Tyr Lys Met Asp Thr Leu Glu Pro Phe Gly Asp Glu Phe Ser
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Gly Met Ala Arg Cys Pro Tyr Asp Ala Lys His Ala Asn Val Ala Leu
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Phe Ala Asp Gly Lys Leu Tyr Ser Ala Thr Val Thr Asp Phe Leu Ala
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Ile Asp Ala Val Ile Tyr Arg Ser Leu Gly Glu Ser Pro Thr Leu Arg
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Thr Val Lys His Asp Ser Lys Trp Leu Lys Glu Pro Tyr Phe Val Gln
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Ala Val Asp Tyr Gly Asp Tyr Ile Tyr Phe Phe Arg Glu Ile Ala
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Val Glu Tyr Asn Thr Met Gly Lys Val Val Phe Pro Arg Val Ala Gln
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Val Cys Lys Asn Asp Met Gly Gly Ser Gln Arg Val Leu Glu Lys Gln
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Trp Thr Ser Phe Leu Lys Ala Arg Leu Asn Cys Ser Val Pro Gly Asp
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Ser His Phe Tyr Phe Asn Ile Leu Gln Ala Val Thr Asp Val Ile Arg
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 Ile Asn Gly Arg Asp Val Val Leu Ala Thr Phe Ser Thr Pro Tyr Asn
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 Lys Phe Leu Ala Arg Ile Gly Asn Ser Gly Phe Leu Asn Asp Ser Leu
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 Gln Thr Gly Leu Ser Lys Arg Leu Glu Met His His Ser Ser Tyr
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His Gln Ala Thr Thr Leu Lys Arg Asn Asn Thr Asn Ser Ser Asn Ser
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Pro Ala Pro Gln Arg Val Asp Ser Ile Gln Val His Ser Ser Gln Pro
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Ser Gly Gln Ala Val Thr Val Ser Arg Gln Pro Ser Leu Asn Ala Tyr
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Asp Val Pro Pro Lys Pro Ser Phe Ala Pro Leu Ser Thr Ser Met Lys
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